

Ref 109 #7

Serial Number:

09/720,529

**ENTERED**

CRF Processing Date: 2/24/2001

Edited by: A

Verified by: (STIC staff)

be

☐

Changed a file from non-ASCII to ASCII

☐

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐

Edited a format error in the Current Application Data section, specifically:

☐

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_

☐

Added the mandatory heading and subheadings for "Current Application Data".

☐

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

☐

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☐

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐

Inserted colons after headings/subheadings. Headings edited included:

☐

Deleted extra, invalid, headings used by an applicant, specifically:

☒

Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_

☐

Inserted mandatory headings, specifically:

☐

Corrected an obvious error in the response, specifically:

☐

Edited identifiers where upper case is used but lower case is required, or vice versa.

☐

Corrected an error in the Number of Sequences field, specifically:

☐

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐

Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected:

☐

Other:

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/720,529

DATE: 07/24/2001

TIME: 18:10:46

Input Set : A:\Pto.amc

Output Set: N:\CRF3\07242001\I720529.raw

3 <110> APPLICANT: E. I. du Pont de Nemours and Company  
 5 <120> TITLE OF INVENTION: Chromatin Associated Proteins  
 7 <130> FILE REFERENCE: BB-1118-A  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/720,529  
 C--> 10 <141> CURRENT FILING DATE: 2001-06-04  
 12 <150> PRIOR APPLICATION NUMBER: 60/092,841  
 13 <151> PRIOR FILING DATE: 1998-07-14  
 15 <160> NUMBER OF SEQ ID NOS: 8  
 17 <170> SOFTWARE: Microsoft Office 97  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 1990  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Oryza sativa  
 24 <400> SEQUENCE: 1

25 gctactttcta cgacgcggag gtgggggaact actactacgg gcagggggcac ccgatgaagc 60  
 26 cgcaccgcat ccgatgacc cagcgctgc tcgccacta cggcctcctc gaccagatgc 120  
 27 aggtgctcaa gccccaccg gcgcgcgacc gcgaccttg ccgcttcac gccgacgact 180  
 28 acgtgcctt cctccgctcc gtcacgcgg agaccagca ggaccagatc cgggcgctca 240  
 29 agcgcttcaa cgtcggcgag gactgccccg tcttcgacgg cctctacagc ttctgccaga 300  
 30 cctacgcgg gggatccgtc ggcggcgcgg tcaagctcaa ccacggccac gacatcgcca 360  
 31 tcaactgggc cggcgccctc caccacgcca agaagtgcga ggctcggga ttctgctacg 420  
 32 tcaacgacat cgctctcgcc atctctgagc tctcaaata ccaccagct gttctctatg 480  
 33 tggatataca tatccacct ggggatggg tggaggagg gttctacagc acggacaggg 540  
 34 tgatgacggg ctggttcac aagtttggg attatttccc ggggaccggg gacattcgcg 600  
 35 atattgggca ctcaaaggg aagtattact ctctgaatgt cccgttggac gacggtatcg 660  
 36 acgacgagag ctaccagtcg ttgttcaagc cgatcatggg gaaggtgatg gaggtttttc 720  
 37 gccctggcgc ggtggtgctc cagtgcgggtg cggactctct gtcgggtgat aggttggggt 780  
 38 gcttcaacct gtcaatcagg ggcacgcgg aatgcgtgag attcatgagg tcttcaatg 840  
 39 tcccgtgtt gctgcttggg ggtggtgggt ataccataag aaatgttgcg cgtgttggt 900  
 40 gctatgagac aggagttgca cttggtcatg agctcactga caagatgcct ccaaatgagt 960  
 41 attttgagta ctttggcca gattatacac ttcattgttc accaagtaac atggagaaca 1020  
 42 aaaacacacg ccagcagttg gatgatataa gatcaagact tcttgataat ctttcaaac 1080  
 43 ttcgacatgc tcctagcgtc caatttcaag agcgaccccc tgaggctgag ctacctgagc 1140  
 44 aagatgaaga ccaagaggat cctgatgaaa ggcaccatgc tgattctgat gtggaaatgg 1200  
 45 atgatgtcaa acctttgat gactcaggaa ggaggagcag tattcagaat gtgagagtta 1260  
 46 agagagagtc tgctgaaaca gatgccgcag atcaggatgg taatagggtc gctgcagaga 1320  
 47 acaccaaggg cacagaacct gcggctgatg gaggttggtc ctcgaaacaa actgttccta 1380  
 48 ccgatgcaag tgcgatggcc atagacgaac caggctccct gaaagtcgag ccagataact 1440  
 49 caaacaatt gcaagatcaa ccacggtgc accagaagac ataatagttc tctctacctt 1500  
 50 aaaacttagt aactgatgcc atctatcatc cattgattat attggagaaa ctcccaactt 1560  
 51 tgaagcagag agttcatgcc ataccaaaag ttatatacca aatttcgaat ggtatgtaca 1620  
 52 cctttcgaac tgggtggtgt ttgtgcaata catttatgcc aggtgacta ttatgtggta 1680  
 53 tctattatta gctttagttt aacctgtct gctgtcagc aatcggtata gtcgtgcaat 1740  
 54 atattctgga tctatcaagc aatgtgagac ggatgtcaaa ccattgggtg tgacttcagc 1800  
 55 aatgtatgta tatgtaagta tagggacagg cagcaggcgt tactttgggt gaagctacaa 1860  
 56 gctttgtctc tcttctcatc cctaatacct acgtggggtg cgtctcggtt ttgttaggt 1920  
 57 attactgcat tcttaaaagt gctcatttag ggtgaaattc taacatcttc taacatactc 1980

RAW SEQUENCE LISTING  
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DATE: 07/24/2001  
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Input Set : A:\Pto.amc  
 Output Set: N:\CRF3\07242001\I720529.raw

1990

```

58 aaaaaaaaaa
60 <210> SEQ ID NO: 2
61 <211> LENGTH: 493
62 <212> TYPE: PRT
63 <213> ORGANISM: Oryza sativa
65 <400> SEQUENCE: 2
66 Tyr Phe Tyr Asp Ala Glu Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His
67   1           5           10           15
69 Pro Met Lys Pro His Arg Ile Arg Met Thr His Ala Leu Leu Ala His
70           20           25           30
72 Tyr Gly Leu Leu Asp Gln Met Gln Val Leu Lys Pro His Pro Ala Arg
73           35           40           45
75 Asp Arg Asp Leu Cys Arg Phe His Ala Asp Asp Tyr Val Ala Phe Leu
76           50           55           60
78 Arg Ser Val Thr Pro Glu Thr Gln Gln Asp Gln Ile Arg Ala Leu Lys
79   65           70           75           80
81 Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Tyr Ser
82           85           90           95
84 Phe Cys Gln Thr Tyr Ala Gly Gly Ser Val Gly Gly Ala Val Lys Leu
85           100          105          110
87 Asn His Gly His Asp Ile Ala Ile Asn Trp Ala Gly Gly Leu His His
88           115          120          125
90 Ala Lys Lys Cys Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val
91           130          135          140
93 Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Val
94   145          150          155          160
96 Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr
97           165          170          175
99 Thr Asp Arg Val Met Thr Val Ser Phe His Lys Phe Gly Asp Tyr Phe
100          180          185          190
102 Pro Gly Thr Gly Asp Ile Arg Asp Ile Gly His Ser Lys Gly Lys Tyr
103          195          200          205
105 Tyr Ser Leu Asn Val Pro Leu Asp Asp Gly Ile Asp Asp Glu Ser Tyr
106          210          215          220
108 Gln Ser Leu Phe Lys Pro Ile Met Gly Lys Val Met Glu Val Phe Arg
109   225          230          235          240
111 Pro Gly Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly Asp
112          245          250          255
114 Arg Leu Gly Cys Phe Asn Leu Ser Ile Arg Gly His Ala Glu Cys Val
115          260          265          270
117 Arg Phe Met Arg Ser Phe Asn Val Pro Leu Leu Leu Leu Gly Gly Gly
118          275          280          285
120 Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Cys Tyr Glu Thr Gly
121          290          295          300
123 Val Ala Leu Gly His Glu Leu Thr Asp Lys Met Pro Pro Asn Glu Tyr
124   305          310          315          320
126 Phe Glu Tyr Phe Gly Pro Asp Tyr Thr Leu His Val Ala Pro Ser Asn
127          325          330          335
129 Met Glu Asn Lys Asn Thr Arg Gln Gln Leu Asp Asp Ile Arg Ser Arg

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```

130          340          345          350
132 Leu Leu Asp Asn Leu Ser Lys Leu Arg His Ala Pro Ser Val Gln Phe
133          355          360          365
135 Gln Glu Arg Pro Pro Glu Ala Glu Leu Pro Glu Gln Asp Glu Asp Gln
136          370          375          380
138 Glu Asp Pro Asp Glu Arg His His Ala Asp Ser Asp Val Glu Met Asp
139 385          390          395          400
141 Asp Val Lys Pro Leu Asp Asp Ser Gly Arg Arg Ser Ser Ile Gln Asn
142          405          410          415
144 Val Arg Val Lys Arg Glu Ser Ala Glu Thr Asp Ala Ala Asp Gln Asp
145          420          425          430
147 Gly Asn Arg Val Ala Ala Glu Asn Thr Lys Gly Thr Glu Pro Ala Ala
148          435          440          445
150 Asp Gly Val Gly Ser Ser Lys Gln Thr Val Pro Thr Asp Ala Ser Ala
151          450          455          460
153 Met Ala Ile Asp Glu Pro Gly Ser Leu Lys Val Glu Pro Asp Asn Ser
154 465          470          475          480
156 Asn Lys Leu Gln Asp Gln Pro Ser Val His Gln Lys Thr
157          485          490
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 1805
161 <212> TYPE: DNA
162 <213> ORGANISM: Glycine max
164 <400> SEQUENCE: 3
165 ctactgcact ctgacactat cagatatcaa tttcagaggg ggactggagg ctggagctgc 60
166 ttcaagtcctt caactatctg aatttctgaa ctcatccatt cgtagcgca stagaacgaa 120
167 aactgagtaa tggaaagtgg agggaaactcc cttccatcag ggtcagatgg tgtgaagaga 180
168 aaggtttcat atttctatga tccagagggt ggaaactatt attatgggca gggacaccca 240
169 atgaaaccac acaggattcg aatgacacat gctcttttag cccactatgg attgcttcaa 300
170 cacatgcagg ttctgaagcc tatggctgct aaagataggg acctttgcaa gttccatgct 360
171 gatgattatg tggcctttct gagaggcatc acccctgaaa cgcagcaaga tcaattgaga 420
172 cagctgaaga ggtttaatgt tggcgaagac tgccctgtat ttgatggtct ttactcttct 480
173 tgccagacat atgcaggagg ttctgttggt ggtgctctaa agttgaacca tggagtatgt 540
174 gatattgcaa taaattgggc tgggtggtcta catcatgcaa agaagtgtga ggcttctggg 600
175 ttttgctatg ttaatgacat tgtgctggct attttggaac ttctcaaaat acatgagcgt 660
176 gttctgtatg tggacattga tatccaccat ggtgatggtg tagaggaggc cttttacacc 720
177 accgataggg tcatgactgt ttcgtttcat aagtttgggg attactttcc tggacaggt 780
178 gatattcgtg atattggata tgctaaaggg aaatattatt cactaaatgt tcccttggat 840
179 gatgaattg atgatgagag ctatcagtc ttgtttaagc caataatggg aaagggtatg 900
180 gagattttta ggcccgggtg tgttgattta caatgtggtg ctgactcttt atctggggac 960
181 aggttaggtt gtttcaatct ttccataaaa ggtcatgcag agtgtgtcag atatatgaga 1020
182 tcttttaatg ttccccttct attgctcggg ggaggtggct atacaataag aaatgtggca 1080
183 cgttgttggt gtttcgagac tagcgttgct cttgggattg aactagatga taagatgcct 1140
184 caacatgaat attatgaata ttttggtcct gactatactc ttcatgttgc tccaagtaac 1200
185 atggaaaaca agaactcccg acaattattg gatgaaataa gagcaaaact tcttgataat 1260
186 ttatctaggc ttcaacatgc accaagtgtc ccattccagg aacggccacc tgatgcagag 1320
187 cttctagaga gagatgaaga tcaagatgat agagatgaaa gatgggatcc cgattctgac 1380
188 agrgaggttg gcgatgacag caatcctgtt cgcagaaggg tgaaaagtga atgcgttgat 1440
189 gctgaggata aagatacagt gtcggggggt gactcaatgg cagtggatga accatgcac 1500

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```

190 aaagaggagc aggataatTTT aaaagagcTT tctgatcaca ggccaagatg aagcaataat 1560
191 aagcattact gatcaacCTT ctccttgact agtgtctgtc gacctgtaaa ttatagtTTC 1620
192 ctcctaaagc agtctggcat gcattcatct gacgtctgta gtgtttcaaa tttttgcttt 1680
193 atctggaaac tgaagagata tggTGcaagc ttgccttggc ttttgatgtt tcatattact 1740
194 gcaagatgaa tgtagtagtt attttttctg taaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1800
195 aaaaaa 1805
197 <210> SEQ ID NO: 4
198 <211> LENGTH: 473
199 <212> TYPE: PRT
200 <213> ORGANISM: Glycine max
202 <400> SEQUENCE: 4
203 Met Glu Ser Gly Gly Asn Ser Leu Pro Ser Gly Ser Asp Gly Val Lys
204 1 5 10 15
206 Arg Lys Val Ser Tyr Phe Tyr Asp Pro Glu Val Gly Asn Tyr Tyr Tyr
207 20 25 30
209 Gly Gln Gly His Pro Met Lys Pro His Arg Ile Arg Met Thr His Ala
210 35 40 45
212 Leu Leu Ala His Tyr Gly Leu Leu Gln His Met Gln Val Leu Lys Pro
213 50 55 60
215 Met Ala Ala Lys Asp Arg Asp Leu Cys Lys Phe His Ala Asp Asp Tyr
216 65 70 75 80
218 Val Ala Phe Leu Arg Gly Ile Thr Pro Glu Thr Gln Gln Asp Gln Leu
219 85 90 95
221 Arg Gln Leu Lys Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp
222 100 105 110
224 Gly Leu Tyr Ser Phe Cys Gln Thr Tyr Ala Gly Gly Ser Val Gly Gly
225 115 120 125
227 Ala Leu Lys Leu Asn His Gly Val Cys Asp Ile Ala Ile Asn Trp Ala
228 130 135 140
230 Gly Gly Leu His His Ala Lys Lys Cys Glu Ala Ser Gly Phe Cys Tyr
231 145 150 155 160
233 Val Asn Asp Ile Val Leu Ala Ile Leu Glu Leu Leu Lys Ile His Glu
234 165 170 175
236 Arg Val Leu Tyr Val Asp Ile Asp Ile His His Gly Asp Gly Val Glu
237 180 185 190
239 Glu Ala Phe Tyr Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys
240 195 200 205
242 Phe Gly Asp Tyr Phe Pro Gly Thr Gly Asp Ile Arg Asp Ile Gly Tyr
243 210 215 220
245 Ala Lys Gly Lys Tyr Tyr Ser Leu Asn Val Pro Leu Asp Asp Gly Ile
246 225 230 235 240
248 Asp Asp Glu Ser Tyr Gln Ser Leu Phe Lys Pro Ile Met Gly Lys Val
249 245 250 255
251 Met Glu Ile Phe Arg Pro Gly Ala Val Val Leu Gln Cys Gly Ala Asp
252 260 265 270
254 Ser Leu Ser Gly Asp Arg Leu Gly Cys Phe Asn Leu Ser Ile Lys Gly
255 275 280 285
257 His Ala Glu Cys Val Arg Tyr Met Arg Ser Phe Asn Val Pro Leu Leu
258 290 295 300

```

## RAW SEQUENCE LISTING

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Input Set : A:\Pto.amc

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```

260 Leu Leu Gly Gly Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp
261 305                               310                               315                               320
263 Cys Phe Glu Thr Ser Val Ala Leu Gly Ile Glu Leu Asp Asp Lys Met
264                               325                               330                               335
266 Pro Gln His Glu Tyr Tyr Glu Tyr Phe Gly Pro Asp Tyr Thr Leu His
267                               340                               345                               350
269 Val Ala Pro Ser Asn Met Glu Asn Lys Asn Ser Arg Gln Leu Leu Asp
270                               355                               360                               365
272 Glu Ile Arg Ala Lys Leu Leu Asp Asn Leu Ser Arg Leu Gln His Ala
273                               370                               375                               380
275 Pro Ser Val Pro Phe Gln Glu Arg Pro Pro Asp Ala Glu Leu Leu Glu
276 385                               390                               395                               400
278 Arg Asp Glu Asp Gln Asp Asp Arg Asp Glu Arg Trp Asp Pro Asp Ser
279                               405                               410                               415
281 Asp Arg Glu Val Gly Asp Asp Ser Asn Pro Val Arg Arg Arg Val Lys
282                               420                               425                               430
284 Ser Glu Cys Val Asp Ala Glu Asp Lys Asp Thr Val Ser Gly Val Asp
285                               435                               440                               445
287 Ser Met Ala Val Asp Glu Pro Cys Ile Lys Glu Glu Gln Asp Asn Leu
288                               450                               455                               460
290 Lys Glu Leu Ser Asp His Arg Pro Arg
291 465                               470
293 <210> SEQ ID NO: 5
294 <211> LENGTH: 541
295 <212> TYPE: DNA
296 <213> ORGANISM: Triticum aestivum
298 <220> FEATURE:
299 <221> NAME/KEY: unsure
300 <222> LOCATION: (134)
302 <220> FEATURE:
303 <221> NAME/KEY: unsure
304 <222> LOCATION: (387)
306 <220> FEATURE:
307 <221> NAME/KEY: unsure
308 <222> LOCATION: (417)
310 <220> FEATURE:
311 <221> NAME/KEY: unsure
312 <222> LOCATION: (433)
314 <220> FEATURE:
315 <221> NAME/KEY: unsure
316 <222> LOCATION: (464)
318 <220> FEATURE:
319 <221> NAME/KEY: unsure
320 <222> LOCATION: (475)
322 <220> FEATURE:
323 <221> NAME/KEY: unsure
324 <222> LOCATION: (479)
326 <220> FEATURE:
327 <221> NAME/KEY: unsure

```

fyt

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/720,529

DATE: 07/24/2001

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Input Set : A:\Pto.amc

Output Set: N:\CRF3\07242001\I720529.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:341 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:345 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:346 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:347 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:371 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6  
L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:386 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6  
L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:389 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6  
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6